Author index

Aitken, E.A.B., Callow, J.A. and Newbury, H.J. *Mutagenesis of a race-specific rust resistance in* Antirrhinum majus *using a transposon-tagging protocol* 775
Albani, D., Sardana, R., Robert, L.S., Altosaar, I., Arnison, P.G. and Fabijanski, S.F. *A* Brassica napus *gene family which shows sequence similarity to ascorbate oxidase is expressed in developing pollen. Molecular characterization and analysis of promoter activity in transgenic tobacco plants* 331
Albericio, F. *see* Ludevid, M.D.
Albersheim, P. *see* Toubart, P.
Albertsen, M. *see* Fauron, C.M.-R.
Altosaar, I. *see* Albani, D.
Alvarez, J., Guli, C.L., Yu, X.-H. and Smyth, D.R. terminal flower: *a gene affecting inflorescence development in* Arabidopsis thaliana 103
Amati, S. *see* Lorberth, R.
Amrhein, N. *see* Schmid, J.
Aotsuka, S. *see* Uchimiya, H.
Argüello, G., García-Hernández, E., Sánchez, M., Gariglio, P., Herrera-Estrella, L. and Simpson, J. *Characterization of DNA sequences that mediate nuclear protein binding to the regulatory region of the* Pisum sativum *(pea) chlorophyll a/b binding protein gene* AB80*: identification of a repeated heptamer motif* 301
Arnison, P.G. *see* Albani, D.
Atanassova, R., Chaubet, N. and Gigot, C. *A 126 bp fragment of a plant histone gene promoter confers preferential expression in meristems of transgenic* Arabidopsis 291
Atherly, A.G. *see* Honeycutt, R.J.

Bako, L. *see* Campos, N.
Baldwin, T.C., Coen, E.S. and Dickinson, H.G. *The* ptl1 *gene expressed in the transmitting tissue of* Antirrhinum *encodes an extensin-like protein* 733
Baltz, R., Domon, C., Pillay, D.T.N. and Steinmetz, A. *Characterization of a pollen-specific cDNA sunflower encoding a zinc finger protein* 713
Banks, P. *see* Goring, D.R.
Barzen, E., Mechelke, W., Ritter, E., Seitzer, J.F. and Salamini, F. *RFLP markers for sugar beet breeding: chromosomal linkage maps and location of major genes for rhizomania resistance, monogermy and hypocotyl colour* 601
Baszczynski, C.L. *see* Goring, D.R.
Batschauer, A. *see* Frohnmeyer, H.
Baulcombe, D. *see* Cejudo, F.J.
Baulcombe, D. *see* Chapman, S.
Bäumlein, H., Nagy, I., Villarroel, R., Inzé, D. and Wobus, U. Cis*-analysis of a seed protein gene promoter: the conservative RY repeat CATGCATG within the legumin box is essential for tissue-specific expression of a legumin gene* 233
Belzile, F. and Yoder, J.I. *Pattern of somatic transposition in a high copy* Ac *tomato line* 173
Bennett, M.D. *see* Parokonny, A.S.
Bergmann, C. *see* Toubart, P.
Bernier, F. *see* Broadhvest, J.
Beven, A.F. *see* Traas, J.A.
Beversdorf, W.D. *see* Goring, D.R.
Bhattacharyya, M. *see* Dry, I.
Birch, R.G. *see* Bower, R.
Bird, C. *see* Bramley, P.
Bisaro, D. *see* Kanevski, I.F.
Bisseling, T. *see* Yang, W.-C.
Blain, I. *see* Bramley, P.
Boll, W. *see* Schmid, J.
Bollini, R. *see* D'Amico, L.
Bonfante-Fasolo, P. *see* Rae, A.L.
Bosnes, M., Weidemann, F. and Olsen, O.-A. *Endosperm differentiation in barley wild-type and* sex *mutants* 661
Bossinger, G., Maddaloni, M., Motto, M. and Salamini, F. *Formation and cell lineage patterns of the shoot apex of maize* 311
Boulton, E.L. *see* Bowsher, C.G.
Boutin, J.-P. *see* Vaucheret, H.
Bower, R. and Birch, R.G. *Transgenic sugarcane plants via microprojectile bombardment* 409
Bowsher, C.G., Boulton, E.L., Rose, J., Nayagam, S. and Emes, M.J. *Reductant for glutamate synthase is generated by the oxidative pentose phosphate pathway in non-photosynthetic root plastids* 893
Bramley, P., Teulieres, C., Blain, I., Bird, C. and Schuch, W. *Biochemical characterization of transgenic tomato plants in which carotenoid synthesis has been inhibited through the expression of antisense RNA to pTOM5* 343
Brandt, J., Thordal-Christensen, H., Vad, K., Gregersen, P.L. and Collinge, D.B. *A pathogen-induced gene of barley encodes a protein showing high similarity to a protein kinase regulator* 815
Brettschneider, R. *see* Langridge, P.
Brewin, N.J. *see* Rae, A.L.
Broadhvest, J., Daigle, N., Martin, M., Haughn, G.W. and Bernier, F. *Appendix: a novel type of homeotic mutation affecting floral morphology* 991
Brosnan, J.M. *see* Johannes, E.
Brough, C. *see* Kanevski, I.F.
Brouwer, M. *see* van der Meer, I.M.
Brown, J.W.S. *see* Simpson, C.G.
Burd, C.G. *see* Ludevid, M.D.
Burow, M.D., Sen, P., Chlan, C.A. and Murai, N. *Developmental control of the β-phaseolin gene requires positive, negative, and temporal seed-specific transcriptional regulatory elements and a negative element for stem and root expression* 537

Caboche, M. *see* Vaucheret, H.
Callow, J.A. *see* Aitken, E.A.B.
Camara, B. *see* Kuntz, M.
Campos, N., Bako, L., Feldwisch, J., Schnell, J. and Palme, K. *A protein from maize labeled with azido-IAA has novel β-glucosidase activity* 675
Canter Cremers, H.C.J. *see* Yang, W.-C.
Carbonell, J. *see* Granell, A.
Casper, M. *see* Fauron, C.M.-R.
Cejudo, F.J., Murphy, G., Chinoy, C. and Baulcombe, D.C. *A gibberellin-regulated gene from wheat with sequence homology to cathepsin B of mammalian cells* 937
Ceriotti, A. *see* D'Amico, L.
Cervone, F. *see* Toubart, P.
Chapman, S., Kavanagh, T. and Baulcombe, D. *Potato virus X as a vector for gene expression in plants* 549
Chaubet, N. *see* Atanassova, R.
Chinoy, C. *see* Cejudo, F.J.

Chlan, C.A. *see* Burow, M.D.
Christou, P. and McCabe, D.E. *Prediction of germ-line transformation events in chimeric R_0 transgenic soybean plantlets using tissue-specific expression patterns* 283
Christou, P. *Genetic transformation of crop plants using microprojectile bombardment* 275
Chua, N.-H. *see* de Pater, B.S.
Coen, E.S. *see* Baldwin, T.C.
Collinge, D.B. *see* Brandt, J.
Conrath, U. *see* Kauss, H.
Cordewener, J. *see* Traas, J.A.
Cosowsky, L. *see* Kanevski, I.F.
Craig, S. *see* Wandelt, C.I.
Creissen, G., Edwards, E.A., Enard, C., Wellburn, A. and Mullineaux, P. *Molecular characterization of glutathione reductase cDNAs from pea (*Pisum sativum *L.)* 129

D'Amico, L., Valsasina, B., Daminati, M.G., Fabbrini, M.S., Nitti, G., Bollini, R., Ceriotti, A. and Vitale, A. *Bean homologs of the mammalian glucose-regulated proteins: induction by tunicamycin and interaction with newly synthesized seed storage proteins* 443
Daigle, N. *see* Broadhvest, J.
Daminati, M.G. *see* D'Amico, L.
Dammann, C. *see* Lorberth, R.
Dangl, J.L. *The major histocompatibility complex à la carte: are there analogies to plant disease resistance genes on the menu?* 3
Daroda, L. *see* Toubart, P.
Darvill, A.G. *see* Toubart, P.
Day, C.D. *see* Winning, B.M.
Dean, C., Sjodin, C., Page, T., Jones, J. and Lister, C. *Behaviour of the maize transposable element* Ac *in* Arabidopsis thaliana 69
De Block, M. and Debrouwer, D. In-situ *enzyme histochemistry on plastic-embedded plant material. The development of an artefact-free β-glucuronidase assay* 261
Debrouwer, D. *see* De Block, M.
de Bruijn, F.J. *see* Dehio, C.
Dehio, C. and de Bruijn, F.J. *The early nodulin gene* SrEnod2 *from* Sesbania rostrata *is inducible by cytokinin* 117
Delcasso-Tremousaygue, D. *see* Echeverria, M.
De Lorenzo, G. *see* Toubart, P.
Delseny, M. *see* Echeverria, M.
Deng, X.-W. and Quail, P. *Genetic and phenotypic characterization of* cop1 *mutants of* Arabidopsis thaliana 83
de Pater, B.S., van der Mark, F., Rueb, S., Katagiri, F., Chua, N.-H., Schilperoort, R.A. and Hensgens, L.A.M. *The promoter of the rice gene* GOS2 *is active in various different monocot tissues and binds rice nuclear factor ASF-1* 837
Desiderio, A. *see* Toubart, P.
de Vienne, D. *see* Downing, W.L.
de Vries, S.C. *see* Fleming, A.J.
De Wit, P.J.G.M. *see* Van den Ackerveken, G.F.J.M.
Dickinson, H.G. *see* Baldwin, T.C.
Dixon, R.A. *see* Shorrosh, B.S.
Domon, C. *see* Baltz, R.
Doonan, J.H. *see* Traas, J.A.
Döring, H.-P. *see* Ott, T.
Downing, W.L., Mauxion, F., Fauvarque, M.-O., Reviron, M.-P., de Vienne, D., Vartanian, N. and Giraudat, J. *A* Brassica napus *transcript encoding a protein related to the Künitz protease inhibitor family accumulates upon water stress in leaves, not in seeds* 685
Draper, J. *see* Hodge, R.
Dreyfuss, G. *see* Ludevid, M.D.
Driouich, A., Laine, A.-C., Vian, B. and Faye, L. *Characterization and localization of laccase forms in stem and cell cultures of sycamore* 13
Dry, I., Smith, A., Edwards, A., Bhattacharyya, M., Dunn, P. and Martin, C. *Characterization of cDNAs encoding two isoforms of granule-bound starch synthase which show differential expression in developing storage organs of pea and potato* 193
Dufour, M.-E. *see* Minet, M.
Dunn, P. *see* Dry, I.

Ebneth, M. *see* Lorberth, R.
Echeverria, M., Delcasso-Tremousaygue, D. and Delseny, M. *A nuclear protein fraction binding to dA/dT-rich sequences upstream from the radish rDNA promoter* 211
Edwards, A. *see* Dry, I.
Edwards, E.A. *see* Creissen, G.
Egeland, D.B. *see* Musci, M.A.
Ehmann, B. *see* Frohnmeyer, H.
Emes, M.J. *see* Bowsher, C.G.
Enard, C. *see* Creissen, G.
Engels, P. and Meyer, P. *Comparison of homologous recombination frequencies in somatic cells of petunia and tobacco suggest two distinct recombination pathways* 59
Epel, B.L. *see* Kotlizky, G.
Espelund, M., Sæboe-Larssen, S., Hughes, D.W., Galau, G.A., Larsen, F. and Jakobsen, K.S. *Late embryogenesis-abundant genes encoding proteins with different numbers of hydrophilic repeats are regulated differentially by abscisic acid and osmotic stress* 241

Fabbrini, M.S. *see* D'Amico, L.
Fabijanski, S.F. *see* Albani, D.
Fallis, L. *see* Goring, D.R.
Fauron, C.M.-R., Casper, M., Gesteland, R. and Albertsen, M. *A multi-recombination model for the mtDNA rearrangements seen in maize cmsT regenerated plants* 949
Fauvarque, M.-O. *see* Downing, W.L.
Faye, L. *see* Driouich, A.
Feldwisch, J. *see* Campos, N.
Fleming, A.J., Mandel, T., Hofmann, S., Sterk, P., de Vries, S.C. and Kuhlemeier, C. *Expression pattern of a tobacco lipid transfer protein gene within the shoot apex* 855
Fluhr, R. *see* Jansen, M.A.K.
Folk, W.R. *see* Franklin, S.
Franklin, F.C.H. *see* Hackett, R.M.
Franklin, S., Lin, T.Y. and Folk, W.R. *Construction and expression of nonsense suppressor tRNAs which function in plant cells* 583
Franssen, H. *see* Yang, W.-C.
Freire, M.A. *see* Ludevid, M.D.
Frohberg, C. *see* Gatz, C.
Frohnmeyer, H., Ehmann, B., Kretsch, T., Rocholl, M., Harter, K., Nagatani, A., Furuya, M., Batschauer, A., Hahlbrock, K. and Schafer, E. *Differential usage of photoreceptors for chalcone synthase gene expression during plant development* 899
Furuya, M. *see* Frohnmeyer, H.
Fütterer, J. *see* Gordon, K.

Galau, G.A. *see* Espelund, M.
Galili, G. *see* Shaul, O.
García-Hernández, E. *see* Argüello, G.

Gariglio, P. *see* Argüello, G.
Gast, R.T. *see* Shi, L.
Gatz, C., Frohberg, C. and Wendenburg, R. *Stringent repression and homogeneous de-repression by tetracycline of a modified CaMV 35S promoter in intact transgenic tobacco plants* 397
Gesteland, R. *see* Fauron, C.M.-R.
Gigot, C. *see* Atanassova, R.
Giralt, E., *see* Ludevid, M.D.
Giraudat, J. *see* Downing, W.L.
Gleba, Y.Y. *see* Parokonny, A.S.
Gómez, J. *see* Ludevid, M.D.
Gopalraj, M. *see* Shi, L.
Gordon, K., Fütterer, J. and Hohn, T. *Efficient initiation of translation at non-AUG triplets in plant cells* 809
Goring, D.R., Banks, P., Fallis, L., Baszczynski, C.L., Beversdorf, W.D. and Rothstein, S.J. *Identification of an S-locus glycoprotein allele introgressed from* B. napus *ssp.* rapfera *to* B. napus *ssp.* oleifera 983
Granell, A., Harris, N., Pisabarro, G. and Carbonell, J. *Temporal and spatial expression of a thiolprotease gene during pea ovary senescence, and its regulation by gibberellin* 907
Gregersen, P.L. *see* Brandt, J.
Guli, C.L. *see* Alvarez, J.
Gustafsson, P. *see* Lidholm, J.

Hackett, R.M., Lawrence, M.J. and Franklin, F.C.H. *A* Brassica *S-locus related gene promoter directs expression in both pollen and pistil of tobacco* 613
Hahlbrock, K. *see* Frohnmeyer, H.
Hahlbrock, K. *see* Schröder, M.
Haigler, C.H. *see* Taylor, J.G.
Halford, N.G., Vincente-Carbajosa, J., Sabelli, P.A., Shewry, P.R., Hannappel, U. and Kreis, M. *Molecular analysis of a barley multigene family homologous to the yeast protein kinase gene* SNF1 791
Hamilton, D.A. *see* Mascarenhas, J.P.
Handberg, K. and Stougaard, J. Lotus japonicus, *an autogamous, diploid legume species for classical and molecular genetics* 487
Hannappel, U. *see* Halford, N.G.
Harris, N. *see* Granell, A.
Harter, K. *see* Frohnmeyer, H.
Hashimoto, H. *see* Uchimiya, H.
Haughn, G.W. *see* Broadhvest, J.
Hensgens, L.A.M. *see* de Pater, B.S.
Herrera-Estrella, L. *see* Argüello, G.
Hetherington, A.M. *see* Masters, A.K.
Higgins, T.J.V. *see* Wandelt, C.I.
Ho, J.Y., Weide, R., Ma, H.M., van Wordragen, M.F., Lambert, K.N., Koornneef, M., Zabel, P. and Williamson, V.M. *The root-knot nematode resistance gene (*Mi*) in tomato: construction of a molecular linkage map and identification of dominant cDNA markers in resistant genotypes* 971
Hodge, R., Paul, W., Draper, J. and Scott, R. *Cold-plaque screening: a simple technique for the isolation of low abundance, differentially expressed transcripts from conventional cDNA libraries* 257
Hofmann, S. *see* Fleming, A.J.
Hogendijk, P. *see* Yang, W.-C.
Hohn, B. *see* Shen, W.-H.
Hohn, T. *see* Gordon, K.
Honeycutt, R.J., Sobral, B.W.S., McClelland, M. and Atherly, A.G. *Analysis of large DNA from soybean (*Glycine max *L. Merr.) by pulsed-field gel electrophoresis* 133
Hughes, D.W. *see* Espelund, M.
Hughes, M.A. *see* Pancoro, A.
Hugueney, P. *see* Kuntz, M.

Inzé, D. *see* Bäumlein, H.

Jackson, D., Roberts, K. and Martin, C. *Temporal and spatial control of expression of anthocyanin biosynthetic genes in developing flowers of* Antirrhinum majus 425
Jakobsen, K.S. *see* Espelund, M.
Jansen, M.A.K., Sessa, G., Malkin, S. and Fluhr, R. *PEPC-mediated carbon fixation in transmitting tract cells reflects style–pollen tube interactions* 507
Johannes, E., Brosnan, J.M. and Sanders, D. *Parallel pathways for intracellular* Ca^{2+} *release from the vacuole of higher plants* 97
Jones, J. *see* Dean, C.

Kamada, I., Yamauchi, S., Youssefian, S. and Sano, H. *Transgenic tobacco plants expressing* rgp1, *a gene encoding a* ras*-related GTP-binding protein from rice, show distinct morphological characteristics* 799
Kandasamy, M.K. *see* Nasrallah, M.
Kanevski, I.F., Thakur, S., Cosowsky, L., Sunter, G., Brough, C., Bisaro, D. and Maliga, P. *Tobacco lines with high copy number of replicating recombinant geminivirus vectors after biolistic DNA delivery* 457
Karrer, E.E. and Rodriguez, R.L. *Metabolic regulation of rice* α*-amylase and sucrose synthase genes* in planta 517
Katagiri, F. *see* Pater, B.S.
Katinakis, P. *see* Yang, W.-C.
Kato, A. *see* Kawai, M.
Kato, A. *see* Uchimiya, H.
Kauss, H., TheisingerHinkel, E., Mindermann, R. and Conrath, U. *Dichloroisonicotinic and salicylic acid, inducers of systemic acquired resistance, enhance fungal elicitor responses in parsley cells* 655
Kavanagh, T. *see* Chapman, S.
Kawagoe, Y. and Murai, N. *Four distinct nuclear proteins recognize* in vitro *the proximal promoter of the bean seed storage protein* β-phaseolin *gene conferring spatial and temporal control* 927
Kawai, M., Kidou, S., Kato, A. and Uchimiya, H. *Molecular characterization of cDNA encoding for adenylate kinase of rice (*Oryza sativa *L.)* 845
Kenton, A.Y. *see* Parokonny, A.S.
Khan, M.R.I. *see* Wandelt, C.I.
Kido, N. *see* Uchimiya, H.
Kidou, S. *see* Kawai, M.
Klessig, D.F. *see* Malamy, J.
Knox, J.P. *Cell adhesion, cell separation and plant morphogenesis* 137
Kombrink, E. *see* Schröder, M.
Komeda, Y. *see* Takahashi, T.
Koonce, L.T. *see* Taylor, J.G.
Koornneef, M. *see* Ho, J.Y.
Kotlizky, G., Shurtz, S., Yahalom, A., Malik, Z., Traub, O. and Epel, B.L. *An improved procedure for the isolation of plasmodesmata embedded in clean maize cell walls* 623
Kreis, M. *see* Halford, N.G.
Kretsch, T. *see* Frohnmeyer, H.
Kronenberger, J. *see* Vaucheret, H.
Kuhlemeier, C. *see* Fleming, A.J.
Kuntz, M., Römer, S., Suire, C., Hugueney, P., Weil, J.H., Schantz, R. and Camara, B. *Identification of a cDNA for the*

plastid-located geranylgeranyl pyrophosphate synthase from Capsicum annuum: *correlative increase in enzyme activity and transcript level during fruit ripening* 25

Lacroute, F. *see* Minet, M.
Laine, A.-C. *see* Driouich, A.
Lambert, K.N. *see* Ho, J.Y.
Langridge, P., Brettschneider, R., Lazzeri, P. and Lörz, H. *Transformation of cereals via* Agrobacterium *and the pollen pathway: a critical assessment* 631
Larsen, F. *see* Espelund, M.
Lawrence, M.J. *see* Hackett, R.M.
Lazzeri, P. *see* Langridge, P.
Leaver, C.J. *see* Winning, B.M.
Leech, R.M. *see* Marrison, J.L.
Leibinger, U. *see* Schmid, J.
Lepingle, A. *see* Vaucheret, H.
Lidholm, J. and Gustafsson, P. *A functional promoter shift of a chloroplast gene: a transcriptional fusion between a novel* psbA *gene copy and the* trnK *(UUU) gene in* Pinus contorta 875
Lin, T.Y. *see* Franklin, S.
Lister, C. *see* Dean, C.
Lorberth, R., Dammann, C., Ebneth, M., Amati, S. and Sánchez-Serrano, J.J. *Promoter elements involved in environmental and developmental control of potato proteinase inhibitor II expression* 477
Lörz, H. *see* Langridge, P.
Luckner, M. *see* Reinbothe, C.
Ludevid, M.D., Freire, M.A., Gómez, J., Burd, C.G., Albericio, F., Giralt, E., Dreyfuss, G. and Pagès, M. *RNA binding characteristics of a 16 kDa glycine-rich protein from maize* 999

Ma, H.M. *see* Ho, J.Y.
Maddaloni, M. *see* Bossinger, G.
Malamy, J. and Klessig, D.F. *Salicylic acid and plant disease resistance* 643
Maliga, P. *see* Kanevski, I.F.
Malik, Z. *see* Kotlizky, G.
Malkin, S. *see* Jansen, M.A.K.
Mandel, T. *see* Fleming, A.J.
Marrison, J.L. and Leech, R.M. *Co-immunolocalization of topoisomerase II and chloroplast DNA in developing, dividing and mature wheat chloroplasts* 783
Martin, C. *see* Dry, I.
Martin, C. *see* Jackson, D.
Martin, M. *see* Broadhvest, J.
Mascarenhas, J.P. and Hamilton, D.A. *Artifacts in the localization of GUS activity in the anthers of petunia transformed with a CaMV 35S–GUS construct* 405
Masson, J. and Paszkowski, J. *The culture response of* Arabidopsis thaliana *protoplasts is determined by the growth conditions of donor plants* 829
Masters, A.K., Shirras, A.D. and Hetherington, A.M. *Maternal mRNA and early development in* Fucus serratus 619
Matsubayashi, Y. *see* Uchimiya, H.
Mauxion, F. *see* Downing, W.L.
McCabe, D.E. *see* Christou, P.
McClelland, M. *see* Honeycutt, R.J.
McCourt, P. *see* Nambara, E.
Mechelke, W. *see* Barzen, E.
Meredith, L. *see* Parokonny, A.S.
Meyer, P. *see* Engels, P.
Meyer, P. *see* Pröls, F.
Miki, B.L. *see* Ouellet, T.
Mindermann, R. *see* Kauss, H.
Minet, M., Dufour, M.-E. and Lacroute, F. *Complementation of* Saccharomyces cerevisiae *auxotrophic mutants by* Arabidopsis thaliana *cDNAs* 417
Mol, J.N.M. *see* van der Meer, I.M.
Motto, M. *see* Bossinger, G.
Mullineaux, P. *see* Creissen, G.
Murai, N. *see* Burow, M.D.
Murai, N. *see* Kawagoe, Y.
Murphy G. *see* Cejudo, F.J.
Musci, M.A., Egeland, D.B. and Schuler, M.A. *Molecular comparison of monocot and dicot U1 and U2 snRNAs* 589

Nagatani, A. *see* Frohnmeyer, H.
Nagy, I. *see* Bäumlein, H.
Naito, S. *see* Nambara, E.
Naito, S. *see* Takahashi, T.
Nambara, E., Naito, S. and McCourt, P. *A mutant of* Arabidopsis *which is defective in seed development and storage protein accumulation is a new* abi3 *allele* 435
Nasrallah, J.B. *see* Nasrallah, M.
Nasrallah, M., Kandasamy, M.K. and Nasrallah, J.B. *A genetically defined* trans*-acting locus regulates* S*-locus function in* Brassica 497
Nayagam, S. *see* Bowsher, C.G.
Nelsen-Salz, B. *see* Ott, T.
Newbury, H.J. *see* Aitken, E.A.B.
Nishi, R. *see* Uchimiya, H.
Nitti, G. *see* D'Amico, L.

Olsen, O.-A. *see* Bosnes, M.
Olszewski, N.E. *see* Shi, L.
Oparka, K.J. and Prior, D.A.M. *Direct evidence for pressure-generated closure of plasmodesmata* 741
Ott, T., Nelsen-Salz, B. and Döring, H.-P. *PCR-aided genomic sequencing of 5′subterminal sequences of the maize transposable element* Activator (Ac) *in transgenic tobacco plants* 705
Ouellet, T., Rutledge, R.G. and Miki, B.L. *Members of the acetohydroxyacid synthase multigene family of* Brassica napus *have divergent patterns of expression* 321
Owen Jr, T.P. *see* Taylor, J.G.
Owens, S.J. *see* Parokonny, A.S.

Page, T. *see* Dean, C.
Pagès, M. *see* Ludevid, M.D.
Palme, K. *see* Campos, N.
Palukaitis, P. *see* Sleat, D.E.
Pancoro, A. and Hughes, M.A. In-situ *localization of cyanogenic* β-glucosidase *(linamarase) gene expression in leaves of cassava (*Manihot esculenta *Cranz) using non-isotopic riboprobes* 821
Parokonny, A.S., Kenton, A.Y., Gleba, Y.Y. and Bennett, M.D. *Genome reorganization in* Nicotiana *asymmetric somatic hybrids analysed by* in situ *hybridization* 863
Parokonny, A.S., Kenton, A.Y., Meredith, L., Owens, S.J. and Bennett, M.D. *Genomic divergence of allopatric sibling species studied by molecular cytogenetics of their* F_1 *hybrids* 695
Paszkowski, J. *see* Masson, J.
Paul, W. *see* Hodge, R.
Pillay, D.T.N. *see* Baltz, R.
Pisabarro, G. *see* Granell, A.

Prior, D.A.M. *see* Oparka, K.J.
Pröls, F. and Meyer, P. *The methylation patterns of chromosomal integration regions influence gene activity of transferred DNA in* Petunia hybrida 465
Purdue, P.E. *see* Winning, B.M.

Quail, P. *see* Deng, X.-W.

Rae, A.L., Bonfante-Fasolo, P. and Brewin, N.J. *Structure and growth of infection threads in the legume symbiosis with* Rhizobium leguminosarum 385
Rawsthorne, S. *C_3–C_4 intermediate photosyntheses: linking physiology to gene expression* 267
Reinbothe, C., Tewes, A., Luckner, M. and Reinbothe, S. *Differential gene expression during somatic embryogenesis in* Digitalis lanata *analyzed by* in vivo *and* in vitro *protein synthesis* 917
Reinbothe, S. *see* Reinbothe, C.
Reviron, M.-P. *see* Downing, W.L.
Ritter, E. *see* Barzen, E.
Robert, L.S. *see* Albani, D.
Roberts, K. *see* Jackson, D.
Rocholl, M. *see* Frohnmeyer, H.
Rodriguez, R.L. *see* Karrer, E.E.
Römer, S. *see* Kuntz, M.
Rose, J. *see* Bowsher, C.G.
Rothstein, S.J. *see* Goring, D.R.
Rueb, S. *see* de Pater, B.S.
Rutledge, R.G. *see* Ouellet, T.

Sabelli, P.A. *see* Halford, N.G.
Sæboe-Larssen, S. *see* Espelund, M.
Salamini, F. *see* Barzen, E.
Salamini, F. *see* Bossinger, G.
Salvi, G. *see* Toubart, P.
Sánchez, M. *see* Argüello, G.
Sánchez-Serrano, J.J. *see* Lorberth, R.
Sanders, D. *see* Johannes, E.
Sano, H. *see* Kamada, I.
Sarah, C.J. *see* Winning, B.M.
Sardana, R. *see* Albani, D.
Scandalios, J.G. *see* Williamson, J.D.
Schafer, E. *see* Frohnmeyer, H.
Schäffner, A.R. and Sheen, J. *Maize C_4 photosynthesis involves differential regulation of phosphoenolpyruvate carboxylase genes* 221
Schaller, A. *see* Schmid, J.
Schantz, R. *see* Kuntz, M.
Schilperoort, R.A. *see* de Pater, B.S.
Schmid, J., Schaller, A., Leibinger, U., Boll, W. and Amrhein, N. *The* in-vitro *synthesized tomato shikimate kinase precursor is enzymatically active and is imported and processed to the mature enzyme by chloroplasts* 375
Schnell, J. *see* Campos, N.
Schröder, M., Hahlbrock, K. and Kombrink, E. *Temporal and spatial patterns of 1,3-β-glucanase and chitinase induction in potato leaves infected by* Phytophthora infestans 161
Schroeder, H.E. *see* Wandelt, C.I.
Schuch, W. *see* Bramley, P.
Schuler, M.A. *see* Musci, M.A.
Scott, R. *see* Hodge, R.
Seitzer, J.F. *see* Barzen, E.
Sen, P. *see* Burow, M.D.
Sessa, G. *see* Jansen, M.A.K.
Shaul, O. and Galili, G. *Increased lysine synthesis in tobacco plants that express high levels of bacterial dihydrodipicolinate synthase in their chloroplasts* 203
Shaw, P.J. *see* Traas, J.A.
Sheen, J. *see* Schaffner, A.R.
Shen, W.-H. and Hohn, B. *Excision of a transposable element from a viral vector introduced into maize plants by agroinfection* 35
Shewry, P.R. *see* Halford, N.G.
Shi, L., Gast, R.T., Gopalraj, M. and Olszewski, N.E. *Characterization of a shoot-specific, GA_3- and ABA-regulated gene from tomato* 153
Shimazaki, T. *see* Uchimiya, H.
Shirras, A.D. *see* Masters, A.K.
Shorrosh, B.S. and Dixon, R.A. *Molecular characterization and expression of an alfalfa protein with sequence similarity to mammalian ERp72, a glucose-regulated endoplasmic reticulum protein containing active site sequences of protein disulphide isomerase* 51
Shurtz, S. *see* Kotlizky, G.
Simpson, C.G., Sinibaldi, R. and Brown, J.W.S. *Rapid analysis of plant gene expression by a novel reverse transcriptase–PCR method* 835
Simpson, J. *see* Argüello, G.
Sinibaldi, R. *see* Simpson, C.G.
Sjodin, C. *see* Dean, C.
Sleat, D.E. and Palukaitis, P. *A single nucleotide change within a plant virus satellite RNA alters the host specificity of disease induction* 43
Smith, A. *see* Dry, I.
Smyth, D.R. *see* Alvarez, J.
Sobral, B.W.S. *see* Honeycutt, R.J.
Soll, J. and Waegemann, K. *A functionally active protein import complex from chloroplasts* 253
Sonnewald, U. *Expression of* E. coli *inorganic pyrophosphatase in transgenic plants alters photoassimilate partitioning* 571
Spelt, C.E. *see* van der Meer, I.M.
Spencer, D. *see* Wandelt, C.I.
Steinmetz, A. *see* Baltz, R.
Sterk, P. *see* Fleming, A.J.
Stougaard, J. *see* Handberg, K.
Stuitje, A.R. *see* van der Meer, I.M.
Suire, C. *see* Kuntz, M.
Sunter, G. *see* Kanevski, I.F.

Takahashi, T., Naito, S. and Komeda, Y. *The* Arabidopsis HSP18.2 *promoter/*GUS *gene fusion in transgenic* Arabidopsis *plants: a powerful tool for the isolation of regulatory mutants of the heat-shock response* 751
Takamatsu, S. *see* Uchimiya, H.
Taylor, J.G., Owen Jr, T.P., Koonce, L.T. and Haigler, C.H. *Dispersed lignin in tracheary elements treated with cellulose synthesis inhibitors provides evidence that molecules of the secondary cell wall mediate wall patterning* 959
Teulieres, C. *see* Bramley, P.
Tewes, A. *see* Reinbothe, C.
Thakur, S. *see* Kanevski, I.F.
Theisinger-Hinkel, E. *see* Kauss, H.
Thordal-Christensen, H. *see* Brandt, J.
Toubart, P., Desiderio, A., Salvi, G., Cervone, F., Daroda, L., De Lorenzo, G., Bergmann, C., Darvill, A.G. and Albersheim, P. *Cloning and characterization of the gene encoding the endopolygalacturonase-inhibiting protein (PGIP) of* Phaseolus vulgaris *L.* 367
Traas, J.A., Beven, A.F., Doonan, J.H., Cordewener, J. and

Shaw, P.J. *Cell-cycle-dependent changes in labelling of specific phosphoproteins by the monoclonal antibody MPM-2 in plant cells* 723
Traub, O. *see* Kotlizky, G.
Twell, D. *Use of a nuclear-targeted β-glucuronidase fusion protein to demonstrate vegetative cell-specific gene expression in developing pollen* 887

Uchimiya, H. *see* Kawai, M.
Uchimiya, H., Kido, S., Shimazaki, T., Aotsuka, S., Takamatsu, S., Nishi, R., Hashimoto, H., Matsubayashi, Y., Kido, N., Umeda, M. and Kato A. *Random sequencing of cDNA libraries reveals a variety of expressed genes in cultured cells of rice (*Oryza sativa *L.)* 1005
Umeda, M. *see* Uchimiya, H.

Vad, K. *see* Brandt, J.
Valsasina, B. *see* D'Amico, L.
Van den Ackerveken, G.F.J.M., Van Kan, J.A.L. and De Wit, P.J.G.M. *Molecular analysis of the avirulence gene* avr9 *of the fungal tomato pathogen* Cladosporium fulvum *fully supports the gene-for-gene hypothesis* 359
van der Mark, F. *see* de Pater, B.S.
van der Meer, I.M., Brouwer, M., Spelt, C.E., Mol, J.N.M. and Stuitje, A.R. *The TACPyAT repeats in the chalcone synthase promoter of* Petunia hybrida *act as a dominant negative* cis-*acting module in the control of organ-specific expression* 525
Van Kammen, A. *see* Yang, W.-C.
Van Kan, J.A.L. *see* Van den Ackerveken, G.F.J.M.
van Wordragen, M.F. *see* Ho, J.Y.
Vartanian, N. *see* Downing, W.L.
Vaucheret, H., Kronenberger, J., Lepingle, A., Vilaine, F., Boutin, J.-P. and Caboche, M. *Inhibition of tobacco nitrate reductase activity by expression of antisense RNA* 559
Vian, B. *see* Driouich, A.
Vilaine, F. *see* Vaucheret, H.
Villarroel, R. *see* Bäumlein, H.
Vincente-Carbajosa, J. *see* Halford, N.G.
Vitale, A. *see* D'Amico, L.

Waegemann, K. *see* Soll, J.
Wandelt, C.I., Khan, M.R.I., Craig, S., Schroeder, H.E., Spencer, D. and Higgins, T.J.V. *Vicilin with carboxy-terminal KDEL is retained in the endoplasmic reticulum and accumulates to high levels in the leaves of transgenic plants* 181
Weide, R. *see* Ho, J.Y.
Weidemann, F. *see* Bosnes, M.
Weil, J.H. *see* Kuntz, M.
Wellburn, A. *see* Creissen, G.
Wendenburg, R. *see* Gatz, C.
Wijffelman, C.A. *see* Yang, W.-C.
Williamson, J.D. and Scandalios, J.G. *Differential response of maize catalases and superoxide dismutases to the photoactivated fungal toxin cercosporin* 351
Williamson, V.M. *see* Ho, J.Y.
Winning, B.M. Sarah, C.J., Purdue, P.E., Day, C.D. and Leaver, C.J. *The adenine nucleotide translocator of higher plants is synthesized as a large precursor that is processed upon import into mitochondria* 763
Wobus, U. *see* Bäumlein, H.

Yahalom, A. *see* Kotlizky, G.
Yamauchi, S. *see* Kamada, I.
Yang, W.-C., Canter Cremers, H.C.J., Hogendijk, P., Katinakis, P., Wijffelman, C.A., Franssen, H., Van Kammen, A. and Bisseling, T. In-situ *localization of chalcone synthase mRNA in pea root nodule development* 143
Yoder, J.I. *see* Belzile, F.
Youssefian, S. *see* Kamada, I.
Yu, X.-H. *see* Alvarez, J.

Zabel, P. *see* Ho, J.Y.

Subject index

abscisic acid (ABA) 153, 241, 477, 685, 999
Ac 173
Accell™ 275
actin 619
Activator (*Ac*) 69
adenine nucleotide translocator 763
adenylate kinase 845
ADP/ATP translocase 763
A1 gene 465
Agrobacterium 631, 991
Agrobacterium transformation of *Lotus japonicus* 487
AHAS 321
alfalfa suspension culture 51
allopatric speciation 695
anther 261
anther-specific 257
anthocyanin 425
Antirrhinum 405, 425, 733, 775
antisense RNA 343, 559
apex cell lineages 311
apical dominance 799
Arabidopsis 69, 83, 103, 417, 751, 829
ascorbate oxidase 331
aspartate pathway 203
asymmetric somatic hybrids 863
auxin-binding protein 675
avirulence genes 3

barley 631, 791
  endosperm 661
bean seed storage protein 537
Beta 97
Brassica 261, 331, 497, 613, 685, 983

CACCTG 927
CACGTG 927
calcium channel 97
CaMV 35S 405
  enhancer 525
  promoter 397
carboxy-terminal KDEL 181
carotenoids 25, 343
carrot protoplasts 583
catalase 351
CATATG 927
CAT gene 583
cauliflower mosaic virus 809
cDNA 129, 241, 257, 845
  clone 375, 815
  libraries 417, 1005
  sequence 907
cell
  adhesion 137
  cycle 723
  wall 137, 623, 661
cell-specific expression of glycine decarboxylase 267
cell-wall protein 367
cellulose 959
Cercospora 351
cereals 791
C_4 gene expression 221

chalcone synthase 143, 899
chalcone synthase gene 525
chlorophyll
  a/b binding gene 301
  fluorescence 507
chloroplast
  development 83
  envelope 253, 783
  genome 875
chlorosis induction 43
chromoplast 25
chromosome translocation 601
cis-acting elements 233, 537
CO_2 compensation point 267
complementation 417
  analysis 845
confocal laser scanning microscopy 887
conifer 875
co-ordinate regulation 425
corn 623
coumarin pathway enzymes 655
C_3–C_4 photosyntheses 267
cucumber mosaic virus 43
cultured cells 1005
cyanogenesis 821
cytokinin 117
cytoplasmic male sterility 949
cytoskeleton 723

dA/dT-binding protein 211
dapA 203
de-repression 397
defence response 815
desiccation intolerance 435
determinate growth 103
development 619
developmentally regulated gene 713
2,6-dichlorobenzonitrile 959
2,6-dichloroisonicotinic acid 655
differential distribution of glycine decarboxylase 267
Digitalis 917
dihydrodipicolinate synthase 203
dihydroorotic dehydrogenase 417
disease resistance 161, 643, 971
DNA
  binding proteins 301
  methylation 465, 705
drought 685
Ds1 excision 35

electron transport 507
embryo 193
embryogenesis (somatic) 917
endoplasmic reticulum 181, 443
endosperm syncytium 661
Enod2 117
ERp72 51
Erysiphe 815
exonuclease III protection assay 927
expression 291
  analysis 835

extracellular matrix 137

fertilization 733
flavonoid gene promoters 525
flower 261, 425
  development 103, 733
  expression 477
  morphology 991
Fucus 619
fungal transformation 359

gametophytic 613
gap repair model 59
gel-mobility-shift assay 927
gemini virus vector 457
gene
  cloning 153, 983
  expression 83, 351, 425, 835, 855, 887, 917, 983
  fusion 875
  regulation 117, 153, 233
  transfer 275, 283
genome evolution 695
genomic *in situ* hybridization 695
germination 937
germline transformation 283
gibberellic acids (GAs) 153
gibberellin 435, 937
gib1 mutant 153
β(1–2) glucan 143
glucose-regulated protein 51, 443
β-glucosidase 675, 821
β-glucuronidase 261, 549, 751, 887
glutamate 893
glutathione reductase 129
Glycine 133, 283
glycine decarboxylase 267
glycol methacrylate 261
glycosylation 443
granule-bound starch synthase 193
GT-1 301
GUS 405
gymnosperm 875

heat 751
Helianthus 713
histo-differentiation 661
histochemistry 261
histone promoter 291
homeotic mutant 991
homologous recombination 59
homologous transient expression 221
Hordeum 241, 815
housekeeping (function) 321
hygromycin and kanamycin selection 487

immunocytochemistry 783
immunofluorescence microscopy 723
immunohistochemistry 161
immunolocalization 25
in situ
  hybridization 161, 863, 907
  localization 143, 821
in vitro DNA protein binding 837
inflorescence 103
inorganic pyrophosphatase 571
insertional mutagenesis 991
integration site 465
intercellular space 137
intercellular transport 741
intergenomic translocations 863
intron processing 589
isozyme 845

jasmonic acid 477

Künitz inhibitors 685

leaf primordia formation 311
Lea genes 241
legume root nodules 385
legume seed protein gene 233
leguminosae genetics 487
library screening 257
light
  induction 221
  regulation 83, 301
  response 829
lignin 959
linimarase 821
linkage maps 601
lipid synthesis 855
Lotus regeneration 487
low abundance 257
Lycopersicon 153, 971
lysine overproduction 203

maize 623, 631, 705, 763, 949, 999
  shoot apex 311
  streak virus 35
malate 507
mapping 971
marker segregation 487
maternal mRNA 619
Meloidogyne 971
meristem 291
micro-pressure probe 741
microprojectiles 409
microspore development 331
mitochondria 763
mitochondrial genome 949
monoclonal antibody 137
monocot 221
monogermy 601
MPM-2 723
mRNA 821, 917
multifunctional locus 3
multigene family 791
mutant 103
  screening 751
mutations 83

Nicotiana 507, 613, 855, 863, 991
nitrate reductase 559
nitrite reductase 559
nitrogen fixation 385
nodule 143
nodulin 117
non-isotopic riboprobes 821
nuclear factor ASF-1 837
nuclear matrix 723

nuclear targeting 887
nucleolus organizing regions 695

ORF 809
Oryza 517, 799, 837, 1005
osmotic stress 241
ovary 907
ovule 321
oxidate stress 351
oxidative pentose phosphate pathway 893

parsley suspension cells 655
particle bombardment 275, 283, 837
patch clamp 97
pathogenesis-related proteins 161, 643
pathogenic 43
pattern formation 311
PCR 257
  PCR-aided genomic sequencing 705
pea 193
PEPC multigene family 221
pepper 25
peptide antigen processing 3
Petroselinum 899
Petunia 59, 405, 525
β-phaseolin 537
Phaseolus 385, 443
photoaffinity labelling 675
photoassimilate partitioning 571
photorespiration 267
photosynthesis 301, 507
phylogeny 695
phytochrome 899
phytoene synthase 343
phytohormone-conjugate 675
Pinus 875
Pisum 129, 143, 253, 385, 907
plant
  cell wall 385
  development 83
  disease resistance genes 3
  hormones 435
  nuclei 589
  variegation 311
plant–pathogen interaction 367
plant–pathogen recognition 3
plasma membrane 137
plasmodesmata 623
plasmodesmata-associated proteins 623
plasmodesmatal conductance 741
plastids 893
Poaceae 409
pollen 405, 631, 713, 733, 887
pollen-specific gene 331
polygalacturonase 367
polygalacturonase-inhibiting protein 367
polymerase III 583
position effect 465
potato 193, 763
pre-mRNA splicing 589
prenyltransferases 25
promoter
  analysis 233
  sequence 331
promoter–GUS fusions 525

14-3-3 protein 815
protein 623, 917
  import 253, 763
  kinases 791
  level 181
  phosphorylation 723
protein disulphide isomerase 51
protoplast 133, 221, 829
psbA 875
Puccinia 775
pulsed-field gel electrophoresis 133

rRNA nuclear genes 211
race-specific elicitor 359
race-specific resistance 359
radish 211
RAmy3D 517
random sequencing 1005
rbcS 301
rearrangement 875
receptor-ligand systems 3
recombination 949
regulation 559
replicating vector 457
repression 397
resistance 367
  genes 775
reverse transcriptase–PCR 835
RFLP 971
  mapping 103, 173, 487
  markers 601
rgp1 799
Rhizobium 143
rhizomania resistance 601
rice 845
  promoter 837
RNA
  recombination 549
  virus 549
RNA-binding protein 999
root–knot nematode 971
roots 893
Rubisco 253, 507
rust 775

Saccharum 409
salicylic acid 643, 655
salt stress 241
satellite RNAs 43
scutellar epithelium 517
scutellum 937
secondary metabolics 643
seed 321
  dormancy 435
self-incompatibility 497, 613, 983
self–non-self recognition 3
senescence 907
sensitivity to fungal elicitor 655
Sesbania 117
sex-mutants 661
shikimate kinase 375
shock protein(s) 751
shoot apex 855
  formation 311
signal transduction 643, 815

Sinapis 899
single strand annealing model 59
SLG genes 983
S-locus 497, 983
small GTP-binding protein 799
Solanum 161
somatic and germinal excision 69
soybean 133
spatial control 537
sporophytic 613
Ss2 517
stigma 733
  compatibility factor 497
storage (vacuolar proteins) 443
streptomycin phosphotransferase (SPT) 69
stress 685
structure–function analysis 3
style 733
subgenomic RNAs 549
sucrose 477
  metabolism 791
sugar beet 601
sugarcane 409
superoxide dismutase 351
symbiotic signal 117
systemic acquired resistance 643, 655

TACPyAT 525
T-DNA 69, 991
telomeres 863
temperature stress 751
temporal control 537
termination codons 583
Tet repressor 397
tetracycline 397
thiolprotease 907, 937
tissue culture 829
tissue-specific expression 51, 321
tobacco 457, 559, 887
tomato 173, 343, 375
tomato golden mosaic virus 457
tonoplast 97
topoisomerase II and ctDNA in wheat chloroplasts 783
Tradescantia 405
trans-acting gene 497
transcriptional activator TGA-1a 837
transcriptional and post-transcriptional control 917
transcriptional regulation 845
transformation 59, 275, 409, 613, 631
transformed phenotype 283
transgenic *Arabidopsis* 291
transgenic crop plants 275
transgenic plants 181, 203, 233, 465, 559, 571, 751
transgenic soybean 283
transgenic tobacco 331, 397, 537, 799
transient gene expression 899
transit peptide 203, 375
translational control 809
transposable element Ac 705
transposition 173, 705
transposon tagging 69, 775
trichome 741
$tRNA^{Trp}$ 583
trnK 875
tuber 193
  expression 477
tunicamycin 51, 443
turgor 741

U2B″ 835
uniconazol 435
untranslated leader 809
UsnRNA 835
U1 snRNAs 589
U2 snRNAs 589
UV-B photoreceptor 899

vacuolar protein 181
Vicia 385
vicilin 181
voltage-gating 97

wheat 631
wound induction 477

X-Gluc 405
xylan 959
xylogenesis 959

yeast 417
yeast expression vector 417

Zea 35, 351, 623, 675
zinc finger protein 713